

(FILE 'HOME' ENTERED AT 13:18:28 ON 11 DEC 2007)

FILE 'REGISTRY' ENTERED AT 13:18:47 ON 11 DEC 2007

L1 9 S LSFAEPG/SQSP  
L2 15032 S [LIMV] S [FWY] [AGPST] [ENDQ] [PAGST] [GAPST] /SQSP  
L3 129 S L2 AND SQL<40  
L4 4 S L2 AND SQL=13  
L5 2 S L2 AND SQL=12  
L6 4 S L2 AND SQL=11  
L7 13 S L2 AND SQL=10  
L8 10 S L2 AND SQL=9  
L9 2 S L1 AND SQL=7

FILE 'HCAPLUS' ENTERED AT 13:21:56 ON 11 DEC 2007

L10 2 S L1 AND EPITOPE

=> S ;4  
ENTER LOGIC EXPRESSION, QUERY NAME, OR (END):end  
SEARCH ENDED BY USER

4 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.  
For a list of commands available to you in the current file, enter  
"HELP COMMANDS" at an arrow prompt (=>).

=> S 14 AND EPITOPE  
4 L4  
42073 EPITOPE  
43843 EPITOPES  
63788 EPITOPE  
(EPITOPE OR EPITOPES)  
L11 2 L4 AND EPITOPE

=> S 15 AND EPITOPE  
2 L5  
42073 EPITOPE  
43843 EPITOPES  
63788 EPITOPE  
(EPITOPE OR EPITOPES)  
L12 0 L5 AND EPITOPE

=> S 16 AND EPITOPE  
4 L6  
42073 EPITOPE  
43843 EPITOPES  
63788 EPITOPE  
(EPITOPE OR EPITOPES)  
L13 2 L6 AND EPITOPE

=> S 17 AND EPITOPE  
15 L7  
42073 EPITOPE  
43843 EPITOPES  
63788 EPITOPE  
(EPITOPE OR EPITOPES)  
L14 12 L7 AND EPITOPE

=> S 18 AND EPITOPE  
14 L8  
42073 EPITOPE  
43843 EPITOPES  
63788 EPITOPE

L15 (EPITOPE OR EPITOPES)  
12 L8 AND EPITOPE

# SCORE Search Results Details for Application 10510875 and Search Result 20071207\_165336\_us-10-510-875a-2.dx.rag.

Score Home Page Retrieve Application List SCORE System.Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165336\_us-10-510-875a-2.dx.rag.

Go Back to previous page

US-10-510-875A-2

Perfect score: 13

Sequence: 1 XRRXXXS 6

Scoring table: BLOSUM62DX

Gapopen 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601679884 residues

total number of hits satisfying chosen Parameters: 3405708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_200711:\*

1: geneseqP1980s:\*

2: geneseqP1990s:\*

3: geneseqP2000:\*

4: geneseqP2001:\*

5: geneseqP2002:\*

6: geneseqP2003a:\*

7: geneseqP2003b:\*

8: geneseqP2004a:\*

9: geneseqP2004b:\*

10: geneseqP2005:\*

11: geneseqP2006:\*

12: geneseqP2007:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result : [Query](#)

No.	Score	Match	Length	DB ID	Description
1	13	100.0	6	2 AAR8653	Aar-8653 RGD conta
2	13	100.0	6	2 AAR7255	Aar7255 ADP-ribos
3	13	100.0	6	2 AAR72520	Aar72520 ADP-ribos
4	13	100.0	6	2 AAR70482	Cancer me
5	13	100.0	6	2 AAR864	Peptide f
6	13	100.0	6	2 AAW2285	Urokinase
7	13	100.0	6	2 AAW4361	AAW4361 PKB subst
8	13	100.0	6	2 AAW56919	AAW56919 Enzyme in
9	13	100.0	6	2 AAW8834	Murine BA
10	13	100.0	6	2 AAW8836	Murine BA
11	13	100.0	6	2 AAW58840	Murine BA
12	13	100.0	6	2 AAW8842	Murine BA
13	13	100.0	6	2 AAW8838	Murine BA
14	13	100.0	6	2 AAW8766	Peptide f
15	13	100.0	6	2 AAW61330	BCL-XL/BC
16	13	100.0	6	2 AAW61326	BCL-XL/BC
17	13	100.0	6	2 AAW61324	BCL-XL/BC
18	13	100.0	6	2 AAW61328	BCL-XL/BC
19	13	100.0	6	2 AAW61332	BCL-XL/BC
20	13	100.0	6	2 AAW75357	AAW75357 Hexapepti
21	13	100.0	6	2 AAW75289	AAW75289 Hexapepti
22	13	100.0	6	2 AAW83868	Peptide s
23	13	100.0	6	2 AAY20434	Human mic
24	13	100.0	6	2 AYD20645	Asy20645 Human neu
25	13	100.0	6	2 AAW95206	Peptide f
26	13	100.0	6	2 AAW95201	Peptide f
27	13	100.0	6	2 AAW9886	Peptide S
28	13	100.0	6	2 ADH55030	Adh55030 GP1b/IIa
29	13	100.0	6	2 ADE22445	GP1b/II
30	13	100.0	6	2 AYD23392	V beta 6
31	13	100.0	6	2 AYD21734	Conserved
32	13	100.0	6	2 AYD217423	Human lac
33	13	100.0	6	2 AAY41791	ADP-ribos
34	13	100.0	6	2 AAY41796	Asy41796 ADP-ribos
35	13	100.0	6	2 AYF55251	TCR C HB 1
36	13	100.0	6	2 AYF43355	Asy43355 Pertussis
37	13	100.0	6	3 AYF50637	Alphal-pr
38	13	100.0	6	3 AYF54936	Peptide 1
39	13	100.0	6	3 AYF85997	Human hae
40	13	100.0	6	3 AYF63345	Asy63345 Heat labi
41	13	100.0	6	3 AYF68340	Pertussis
42	13	100.0	6	3 AYF95263	Crostdide
43	13	100.0	6	3 AYF93514	Peptide s
44	13	100.0	6	3 AAB22819	Human lac
45	13	100.0	6	3 AAB08371	Amino aci
46	13	100.0	6	4 AAB49566	Murine Va
47	13	100.0	6	4 AAB66214	B pertussis
48	13	100.0	6	4 AAB65219	E. coli he
49	13	100.0	6	4 AAG67319	Asy67319 Peptide e
50	13	100.0	6	4 AAG67301	Asy67301 Peptide e

## ALIGNMENTS

### RESULT 1

AAR48653

ID

AAR8653

standard

peptide

6 AA.

XK

AC

AAR8653:

XK

DT

25-MAR-2003

(revised)

21-SEP-1994

(first entry)

## SCORE Search Results Details for Application 10510875

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165341\_us-1

Database :		CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 2 of 2			
Title:		Copyright (c) 1993 - 2007 Biocceleration Ltd.			
JW Protein - protein search, using sw model		JW Protein - protein search, using sw model			
Run on:		December 7, 2007, 23:05:54 ; Search time 16 Seconds (without alignments) 35.738 Million cell updates/sec			
Scoring table:		BLOSUM6DX Gap0 10.0 , Gapext 0.5			
Perfect score:		13			
Sequence:		1 XXXXS 6			
Post-processing:		283416 seqs, 96216763 residues			
Total number of hits satisfying chosen parameters:		283416			
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing:		Minimum Match 0% Maximum Match 100%			
Listing first 50 summaries		.			
Database :		PIR_80:*			
1:		pir1:*			
2:		pir2:*			
3:		pir3:*			
4:		pir4:*			
Pred. No.		4			
Score		100.0			
Match		7			
Length		2			
DB		A39650			
ID					
Description					
SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	13	100.0	7	2	A39650
2	13	100.0	7	4	155302
3	13	100.0	8	2	B54833
4	13	100.0	9	2	C57444
5	13	100.0	10	2	B32887
6	13	100.0	11	2	PT0250
7	13	100.0	11	2	PT0302
8	13	100.0	11	2	PH1546
9	13	100.0	11	2	B41946
10	13	100.0	11	2	C38887
11	13	100.0	11	2	A49037
CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 2 of 2					
Copyright (c) 1993 - 2007 Biocceleration Ltd.					
JW Protein - protein search, using sw model					
Run on:					
Scoring table:					
Perfect score:					
Sequence:					
Post-processing:					
Listing first 50 summaries					
Database :					
1:					
2:					
3:					
4:					
Pred. No.					
Score					
Match					
Length					
DB					
ID					
Description					
SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	13	100.0	7	2	A39650
2	13	100.0	7	4	155302
3	13	100.0	8	2	B54833
4	13	100.0	9	2	C57444
5	13	100.0	10	2	B32887
6	13	100.0	11	2	PT0250
7	13	100.0	11	2	PT0302
8	13	100.0	11	2	PH1546
9	13	100.0	11	2	B41946
10	13	100.0	11	2	C38887
11	13	100.0	11	2	A49037
CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 1 of 2					
Copyright (c) 1993 - 2007 Biocceleration Ltd.					
JW Protein - protein search, using sw model					
Run on:					
Scoring table:					
Perfect score:					
Sequence:					
Post-processing:					
Listing first 50 summaries					
Database :					
1:					
2:					
3:					
4:					
Pred. No.					
Score					
Match					
Length					
DB					
ID					
Description					
SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	13	100.0	7	2	A39650
2	13	100.0	7	4	155302
3	13	100.0	8	2	B54833
4	13	100.0	9	2	C57444
5	13	100.0	10	2	B32887
6	13	100.0	11	2	PT0250
7	13	100.0	11	2	PT0302
8	13	100.0	11	2	PH1546
9	13	100.0	11	2	B41946
10	13	100.0	11	2	C38887
11	13	100.0	11	2	A49037
CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 1 of 2					
Copyright (c) 1993 - 2007 Biocceleration Ltd.					
JW Protein - protein search, using sw model					
Run on:					
Scoring table:					
Perfect score:					
Sequence:					
Post-processing:					
Listing first 50 summaries					
Database :					
1:					
2:					
3:					
4:					
Pred. No.					
Score					
Match					
Length					
DB					
ID					
Description					
SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	13	100.0	7	2	A39650
2	13	100.0	7	4	155302
3	13	100.0	8	2	B54833
4	13	100.0	9	2	C57444
5	13	100.0	10	2	B32887
6	13	100.0	11	2	PT0250
7	13	100.0	11	2	PT0302
8	13	100.0	11	2	PH1546
9	13	100.0	11	2	B41946
10	13	100.0	11	2	C38887
11	13	100.0	11	2	A49037
CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 2 of 2					
Copyright (c) 1993 - 2007 Biocceleration Ltd.					
JW Protein - protein search, using sw model					
Run on:					
Scoring table:					
Perfect score:					
Sequence:					
Post-processing:					
Listing first 50 summaries					
Database :					
1:					
2:					
3:					
4:					
Pred. No.					
Score					
Match					
Length					
DB					
ID					
Description					
SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	13	100.0	7	2	A39650
2	13	100.0	7	4	155302
3	13	100.0	8	2	B54833
4	13	100.0	9	2	C57444
5	13	100.0	10	2	B32887
6	13	100.0	11	2	PT0250
7	13	100.0	11	2	PT0302
8	13	100.0	11	2	PH1546
9	13	100.0	11	2	B41946
10	13	100.0	11	2	C38887
11	13	100.0	11	2	A49037
CORE Search Results Details for Application 10510875 and Search Result 20071207_165341_us-10-510... Page 1 of 2					
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## SCORE Search Results Details for Application 10510875 and Search Result 20071207\_165338\_us-10-510-875a-2.dx.rup.

Score.Home.Page Retrieve Application.List SCORE System.Overview SCORE FAQ Comments./ Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165338\_us-10-510-875a-2.dx.rup.

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GenCore version 6.2.1.

77.206 Million cell updates/sec

Title: US-10-510-875A-2

Perfect score: 13

Sequence: 1 XXXXXS 6

Scoring table: BLOSUM62DX

Gapext 10.0 Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : UniProt\_12.1:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	13	100.0	8	1	UH09_RAT	P56575 rattus norvegicus
2	13	100.0	8	2	AON901_RUMAN	AON901 homo sapiens
3	13	100.0	8	2	Q80WDS_MUSPP	Q80WDS mus musculus
4	13	100.0	8	2	Q9QV88_PMURI	Q9QV88 mus musculus
5	13	100.0	8	2	Q89955_POCVJC	Q89955 jc polyomavirus
6	13	100.0	8	2	Q8PU72_SV40	Q8PU72 simian virus 40
7	13	100.0	8	2	Q6QS99_SV40	Q6QS99 simian virus 40
8	13	100.0	8	2	Q8PUD5_SV40	Q8PUD5 simian virus 40

### ALIGNMENTS

#### RESULT 1

QF019\_RAT

Reviewed:

QF019\_RAT

Integrated into UniProtKB/Swiss-Prot.

AC P56575;

DT 15-DEC-1998

Sequence version 1.

DR 24-JUL-2007

entry version 20.

DE Unknown protein from 2D-PAGE of heart tissue (spot P91) (Fragment).

[1]

Rattus norvegicus (Rat)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

NCBI\_TaxID:10116;

RN PROTEIN SEQUENCE.

RC STRAIN=Wildtype; TISSUE=Heart;

RA Li X.-P.; Pleissner K.-P.; Scheeler C.; Regitz-Zagrosek V.; Salikov J.;

Jungblut P.R.;

# SCORE Results Details for Application 10510875 and Search Result 20071207\_165415\_us-10-510-875a-6.rag.

## Score Home Page Retrieve Application List SCORE System.Overview SCORE FAQ Comments./ Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165415\_us-10-510-875a-6.rag.

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US-10-510-875A-6

Perfect score: 36

Sequence: 1 LSFAEFG 7

Scoring table: BLOSUM62

Gapop 11.0 , Gapext 0.5

3405708 seqs, 60187984 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 50 summaries

Database : A\_Geneseq\_200711:\*

1: geneseqP1980s:\*

2: geneseqP1990s:\*

3: geneseqP2000:\*

4: geneseqP2001:\*

5: geneseqP2002:\*

6: geneseqP2003a:\*

7: geneseqP2003b:\*

8: geneseqP2004a:\*

9: geneseqP2004b:\*

10: geneseqP2005:\*

11: geneseqP2007:\*

12: geneseqP2007:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query

<http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3ad0&itemName=200...> 12/11/200

No.	Score	Match	Length	DB	ID	Description
1	36	100.0	7	7	ADE50785	Protein k
2	36	100.0	10	7	ADE50782	Protein k
3	36	100.0	10	7	ADE50786	Protein k
4	36	100.0	10	7	ADE50781	Protein k
5	36	100.0	10	7	ADE50789	Protein k
6	36	100.0	10	12	AEN53756	Kinase no
7	36	100.0	10	12	AFB67165	Substrate
8	36	100.0	11	7	ADE50790	Protein k
9	36	100.0	11	7	ADE50787	Protein k
10	36	100.0	11	7	ADE50788	Protein k
11	36	100.0	11	12	AHS5968	Serine/Thr
12	36	100.0	11	12	AH55989	Serine/Thr
13	36	100.0	13	7	ADE50791	Protein k
14	36	100.0	13	12	AFB67160	Substrate
15	33	91.7	189	10	AEP336370	L. pneumo
16	33	91.7	189	10	AEP339786	L. pneumo
17	33	91.7	484	4	AAB76522	Corynebac
18	33	91.7	491	4	AAB5789	C. Glutam
19	33	91.7	491	4	AAG90675	C. glutami
20	33	91.7	491	6	ADL55551	C. glutam
21	32	88.9	8	5	AAE23344	Human GSK
22	32	88.9	11	5	AAE23345	Human GSK
23	32	88.9	11	11	AET22422	Fluoresce
24	32	88.9	11	11	AET22422	Akt1 assa
25	32	88.9	13	6	ABP54023	Akt speci
26	32	88.9	13	6	ABP54026	Akt speci
27	32	88.9	13	6	AAE29760	Akt speci
28	32	88.9	13	6	AAG79642	Human Akt
29	32	88.9	13	6	ABB39474	Amino aci
30	32	88.9	13	7	AA004278	Akt pepti
31	32	88.9	13	7	ADD96165	Biotin 1a
32	32	88.9	13	7	ADE06653	Peptide s
33	32	88.9	13	7	ADE15867	Peptide s
34	32	88.9	13	7	ADK82126	Akt pepti
35	32	88.9	13	8	AD033600	Biotinylia
36	32	88.9	13	8	AD035205	Human Akt
37	32	88.9	13	8	ADU88697	Akt pepti
38	32	88.9	13	8	AEP4583	Akt pepti
39	32	88.9	13	8	ADU88747	Akt pepti
40	32	88.9	13	8	ADU88568	Akt pepti
41	32	88.9	13	10	AED0288	Akt pepti
42	32	88.9	13	11	AEP27504	CK1K1sv1 k
43	32	88.9	13	11	AEE19201	AKT subst
44	32	88.9	13	11	AE44991	GSK31alpha
45	32	88.9	13	11	AE167776	Human Akt
46	32	88.9	13	11	AEj15815	Checkpoint
47	32	88.9	13	11	AEj15056	Human CTR
48	32	88.9	13	11	AEj0895	Peptide s
49	32	88.9	13	11	AE42820	Akt pepti
50	32	88.9	13	12	AE143685	Human Akt

## ALIGNMENTS

RESULT 1	
ID	ADE50785
XX	
AC	AD55989
XX	
DT	29-JAN-2004 (first entry)
XX	



RA Ventre J.C.;  
 RL Submitted (PEB-2006) to the EMBL/GenBank/DBJ databases.  
 DC :-: CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

DC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 DC Distributed under the Creative Commons Attribution-NoDerivs License  
 DC EMBL: AAO1000002; ECR22003\_1; -; Genomic\_DNA.

DR InterPro: IPR012938; GSDH.  
 DR Pfam: PF0795; GSDH; 1.

SO Predicted; 4: Predicted;

SEQUENCE 372 AA; 40153 MW; 7522PCHA6A526171 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LSFAEPG 7

DB 110 LSFAEPG 116

RESULT 2  
 29IE13\_9HTV2

ID Q9IE13\_9HTV2 Unreviewed; 107 AA.

AC Q9IE13;

DR 01-OCT-2000, integrated into UniProtKB/TrEMBL.

DR 01-OCT-2000, sequence version 1.

DR 24-JUL-2007, entry version 28.

DR Envelope glycoprotein gp105 (Fragment).

NAME=env;

DS Human immunodeficiency virus 2.

DC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

DC Lentivirus; Primate lentivirus group.

DN NCBI\_TaxId:11709;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=00414625; PubMed=10957727; DOI=10.1089/08892220050117069;

RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,

RA Canas-Pereira W.P.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

RL AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

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CC EMBL: AJ246915; CAB95022\_1; -; Genomic\_DNA.

DR GO: 0019031; C:viral envelope; IEA:inter-pro.

DR InterPro: IPR000777; GP120.

DR Gene3D: G3DSA:2.170.40.20; GP120; 1.

DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

FX MEDLINE=00414625;

RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,

RA Canas-Pereira W.P.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

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DR EMBL: AJ246890; CAB95067\_1; -; Genomic\_DNA.

DR GO: GO:0019031; C:viral envelope; IEA:interPro.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

FX MEDLINE=00414625;

RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,

RA Canas-Pereira W.P.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

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DR EMBL: AJ246890; CAB95067\_1; -; Genomic\_DNA.

DR GO: GO:0019031; C:viral envelope; IEA:interPro.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

FX MEDLINE=00414625;

RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,

RA Canas-Pereira W.P.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

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DR EMBL: AJ246890; CAB95067\_1; -; Genomic\_DNA.

DR GO: GO:0019031; C:viral envelope; IEA:interPro.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

FX MEDLINE=00414625;

RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,

RA Canas-Pereira W.P.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

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DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

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DR GO: GO:0019031; C:viral envelope; IEA:interPro.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

PE 4: Predicted;

KW Envelope protein.

FX MEDLINE=00414625;

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RT "Genetic variability of human immunodeficiency virus type 2 C2V3 region within and between individuals from Bissau, Guinea-Bissau, West Africa.";

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DR EMBL: AJ246890; CAB95067\_1; -; Genomic\_DNA.

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DR GO: GO:0019031; C:viral envelope; IEA:interPro.

DR InterPro: IPR000777; GP120; 1.

Score_Home Page Retrieve_Application List SCORE_ System_Overview SCORE FAQ Comments / Suggestions	
This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165425_us-1	
GenCore version 6.2.1	Copyright (c) 1993 - 2007 Biocceleration Ltd.
CCM protein - protein search, using sw model	
Run on: December 7, 2007, 23:12:02 (without alignments)	Search time 39 Seconds
	17.270 Million cell updates/sec
Title: US-10-510-875A-6	
Perfect score: 36	
Sequence: 1 LSFAEFG 7	
Scoring table: BLOSUM62	
Gapop 10.0 , Gapext 0.5	
Searched: 283416 seqs, 96216763 residues	
Total number of hits satisfying chosen parameters:	283416
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	Maximum Match 100%
Listing first 50 summaries	
Database :	PIR 80 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query				Description
	Score	Match Length	DB	ID	
1	33	91.7	223	2	hypothetical protein kinase (EC
2	32	88.9	124	2	protein kinase (EC
3	32	88.9	483	1	ABC1 protein homol
4	31	86.1	623	2	ABC1 protein homol
5	31	86.1	623	2	hypothetical prote
6	21	86.1	2195	2	ovulation hormone
7	30	83.3	259	1	adenylyl methionine
8	30	83.3	360	2	probable carnitine
9	30	83.3	373	2	calcitonin receptor
10	30	83.3	478	2	calcitonin receptor
11	30	83.3	479	2	calcitonin receptor

- 2 -

RESULT 1

H75600 hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: H75600

C;R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.; Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036996; PMID:10567256

A;Accession: H75600

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-223 <WHI>

A;Cross-references: UNIPROT:Q9RZ84; UNIPARC:UPI00000C1610; GB:AE001862; GB:AE001825; NID:95460468; I

A;Experimental source: strain R1

C;Genetics:

A;Gene: DEA0070

A;Mad position: 2

## ALIGNMENTS

			probable amidase
			hypothetical serin
			calcitonin receptor
			chitinase (EC 3.2.1.12)
			hypothetical prote
			ATP-dependent heli
			probable membrane
			genome polyprotein
			genome polyprotein
			hypothetical prote
			hypothetical prote
			hypothetical prote
			acetyl-CoA carboxy
			hypothetical prote
			acetyl-CoA carboxy
			acetyl-CoA carboxy
			acetyl-CoA carboxy
			transcription fact
			hypothetical prote
			UI_SMRNP_70K prote
			1-aminoacyclopropan
			probable acetolact
			acetolactate synth
			hypothetical prote
			probable cAMP- resp
			mammary gland fact
			transcription act1
			mammary gland fact
			1,4-beta-D-glucan
			hypothetical prote
			cellooligosaccharid
			4-alpha-glucanotra
			amylo-alpha-1,6-g1
			low voltage-activa
			phospholase kina
			hypothetical prote
			hypothetical prote
30	83.3	485	2 E83620
30	83.3	485	2 T41714
30	83.3	515	2 I60800
30	83.3	535	2 S65762
30	83.3	727	2 T2585
30	83.3	946	2 F84280
30	83.3	1108	2 T35827
30	83.3	2175	1 GNNYBE
30	83.3	2214	1 A48548
30	83.3	2214	1 G72713
29	80.6	134	2 T21959
29	80.6	258	2 G70001
29	80.6	262	2 G70001
29	80.6	276	2 T08773
29	80.6	282	2 F84045
29	80.6	294	2 AE1251
29	80.6	294	2 AG1533
29	80.6	305	2 T06029
29	80.6	330	2 AH1859
29	80.6	427	2 S71367
29	80.6	431	2 JC7730
29	80.6	515	2 G70806
29	80.6	515	2 S72987
29	80.6	614	2 T23190
29	80.6	617	2 T43059
29	80.6	699	2 T09069
29	80.6	786	2 I49274
29	80.6	793	2 S54772
29	80.6	794	2 G02317
29	80.6	794	2 S55527
29	80.6	821	2 E87303
29	80.6	823	2 B87348
29	80.6	942	2 C96574
29	80.6	980	2 T00045
29	80.6	1515	2 A40203
29	80.6	1556	2 S38758
29	80.6	2254	2 T09053
29	80.6	2254	2 B4431
28	77.8	112	2 S30850
28	77.8	139	2 E75111

	Best Local Matches	Similarity	85.7%	Pred. No.	7.6:	0;	Indels	0;	Gaps	0;
Dy	1	LSFAERG	7							
Db	198	LAFAERG	204							

A: Residues: 1-124 <W00>  
 A: Cross-references: UNIPARC:UPI000017557A  
 C: Superfamily: kinase-related transforming protein; protein kinase homology  
 C: Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F: 39-92/Domain: protein kinase homology (fragments) <KIN>

**RESULT 3**  
**IVRTKA**  
**protein kinase (EC 2.7.1.37) GSK-3-alpha - rat**  
**factor A: glycogen synthase kinase 3 alpha**  
**Alternative names: factor A; glycogen synthase kinase 3 alpha**  
**C.Species: Rattus norvegicus (Norway rat)**  
**C.Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004**  
**C.Accession: S14707**  
**R.Woodgett, J. R.**  
**EMBO J. 9, 2431-2438, 1990**  
**Db**  
**3 SPAEFG**

A;Accession: S14707  
 A;Molecule type: m6NA  
 A;Residues: 1-483 <W00-  
 A;Cross-references: UNIPROT:P18265; UNIPARC:UPI00012DBBP; EMBL:X53427; NID:956331; PIDN:CAA37518\_1;  
 C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: ATP; phosphoprotein; phosphotransferase; seine/threonine-specific protein kinase  
 F;117-378/Domain: protein kinase homology <KIN>  
 F;125-133/Region: protein kinase ATP-binding motif  
 F;148/Active site: Lys #status predicted

Query Match 88.9%; Score 32, DB 1; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 6; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

2 SPAEPG 21 SPAEPG 26

200 2011-07-11 11:11:11

CORE Search Results Details for Application 10510875 and Search Result 20071207 165425 us-10-510... Page 4 of 2

RESULT 4  
T02007 ABC1 protein homolog T15B16.14 - *Arabidopsis thaliana*  
C: Specie: *Arabidopsis thaliana* (mouse-ear cress)  
C: Date: 26-Feb-1999 #sequence\_revision 28-Feb-1999 #text\_change 09-Jul-2004

```

RESULT 4
T02007
  ABC1 protein homolog T15B16.14 - Arabidopsis thaliana
  C;species: Arabidopsis thaliana (mouse-ear cress)
  C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
  C;Accession: T02007
  R;Stoneking, T. / Smith, R.
  R;submitted to the EML Data Library, November 1998
  A;Description: The sequence of A. thaliana T15B16.
  A;Reference number: 214488
  A;Accession: T02007
  A;Status: translated from GB/EMBL/DBS
  A;Molecule type: DNA
  A;Residues: 1-623 <STO>
  A;Cross-references: UNIPROT:Q95BB2; UNIPARC:UPI00000A3E05; EMBL:AP104919; NID:93859590; PID:93859590
  A;Experimental source: cultivar Columbia
  C;Genetics:
  A;Map position: 4
  A;Introns: 182/2; 257/3; 308/3; 361/3; 415/1; 490/3
  A;Note: T15B16.14

Query Match          86.1%; Score: 31; DB: 2; Length: 622;
Best Local Similarity 85.7%; pred. No. 68; 1..740..125

```

2y	1	LSEAEPG	7
Db	533	LPAEPG	539

RESULT 5

ABCI1 protein homolog [imported] - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:ID: 20-10-2000 #sequence\_revision 20-oct-2000  
C:Accession: T52228  
C:Change: 09-Jul-2004

K; DJ JARON, G.  
submitted to the EMBL Data Library, December 1997  
A; Reference number: 225969  
A; Accession: T52128  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
N; Residues: 1-633 <DNA>  
A; Cross-references: UNIPARC:OP10000025AB; EMBL:AJ001158; PIDN:CRA04557.1  
A; Experimental source: ecotype Columbia; seedling  
C; Comments: *Arabidopsis thaliana* (L.) Heynh. (Arabidopsis)

A; Note: ABC1AT	
Query Match	86.1%
Best Local Similarity	88.7%
Matches	6;
Conservative	0;
Mismatches	1;
Indels	0;
Gaps	0;
2y	1 LSPAEPG 7
Db	533 LPPAEPG 539

RESULT 6  
T34264  
hypothetical protein F46C8.4 - *Caenorhabditis elegans*

Comments: [http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=10100000&dopt=Abstract](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=10100000&dopt=Abstract)

<http://www.126.com/zt/2011/12/11/126001.html>

## SCORE Search Results Details for Application 10510875 and Search Result 20071207\_165336\_us-10-510-875a-7.dx.rag.

Score,Home,Page,Retrieve,Application,List,SCORE,System,Overview,SCORE,Comments,/,Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165336\_us-10-510-875a-7.dx.rag.

Go Back to previous page

US-10-510-875A-7

Perfect score: 33

Sequence: 1 LXPFAEPG 7

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0 5

Searched: 3405708 seqs, 60187984 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_200711:\*

1: geneseq1980s:\*

2: geneseq1990s:\*

3: geneseq2000:\*

4: geneseq2001:\*

5: geneseq002:\*

6: geneseq2003a:\*

7: geneseq2003b:\*

8: geneseq0004a:\*

9: geneseq2004b:\*

10: geneseq2005:\*

11: geneseq2006:\*

12: geneseq2007:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## Result

Query

http://es/ScoreAccessWeb/GetItem.action?ApplId=10510875&amp;seqId=09323b67805b3add&amp;itemName=200...

12/11/200...

No.	Score	Match Length	DB ID	Description
1	33	100.0	7	AD50785 Protein k
2	33	100.0	10	AD50782 Protein k
3	33	100.0	10	AD50786 Protein k
4	33	100.0	10	AD50781 Protein k
5	33	100.0	10	AD50789 Protein k
6	33	100.0	10	AEN5756 Kinase no Afb67165 Substrate
7	33	100.0	10	AD50790 Protein k
8	33	100.0	11	AD50790
9	33	100.0	11	AD50787
10	33	100.0	11	AD50788
11	33	100.0	11	AD50788
12	33	100.0	11	AEN5989 Serine/Thr
13	33	100.0	13	AD50791 Protein k
14	33	100.0	13	AD50792 Substrate
15	33	100.0	98	AAU54359 Propionib
16	33	100.0	98	ABM50878 Propionib
17	33	100.0	295	ABM83500 M. xanthu
18	33	100.0	345	AIR46133 Recombina
19	33	100.0	420	ADX77623 Plant ful
20	33	100.0	426	ADY12256 Plant ful
21	33	100.0	426	ADY78935 Plant ful
22	33	100.0	484	ABT7522 Corynebac
23	33	100.0	491	AB45789 C. glutam
24	33	100.0	491	ARG90675 C. glutam
25	33	100.0	491	ADL65551 C. glutam
26	33	100.0	832	AB076120 Pseudomon
27	33	100.0	164	AAW22602 Tytaccone
28	31	93.9	404	AEC95873 Goldfish
29	31	93.9	450	ABM92976 M. xanthu
30	31	93.9	1089	AD91892 Agarase I
31	31	93.9	2195	ADN24175 Bacterial
32	30	90.9	53	ADP10072 Human ORF
33	30	90.9	58	ABD64040 Drosophil
34	30	90.9	68	ABD69113 Drosophil
35	30	90.9	68	AFCL4089 Fruit fly
36	30	90.9	68	AFB9869 Protein fly
37	30	90.9	146	ADP07246 Pseudomon
38	30	90.9	146	ADP96708 Plant ful
39	30	90.9	189	AB353370 L. pneumo
40	30	90.9	189	AB39786 L. pneumo
41	30	90.9	197	ABD5813 Human gen
42	30	90.9	289	AG99376 C. glutam
43	30	90.9	294	ADD13210 C. glutam
44	30	90.9	344	ADP85501 Aspergill
45	30	90.9	353	ABG1721 Novel hum
46	30	90.9	382	ABM86018 Rice abio
47	30	90.9	416	ADN21187 Bacterial
48	30	90.9	430	AES88756 S. agalac
49	30	90.9	430	AES93498 S. agalac
50	30	90.9	430	AES84218 S. agalac

## ALIGNMENTS

RESULT 1	AD50785
ID	AD50785 standard; peptide: 7 AA.
XX	
AC	AD50785;
XX	
DT	29-JAN-2004 (first entry)
XX	

Score\_Home\_Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165341\_us-1

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DBM Protein - Protein search, using sw model

Run on: December 7, 2007, 23:05:54 ; Search time 19 Seconds

(without alignments)  
35.738 Million cell updates/sec

Title: US-10-510-875A-7

Perfect score: 33

Sequence: 1 LXFAEPG 7

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR:80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	33	100.0	223	2	H75600		hypothetical protein
2	33	100.0	623	2	T02007		ABC1 protein homol
3	33	100.0	623	2	TS2128		ABC1 protein homol
4	31	93.9	2175	1	GRNTEBE		genomic polyprotein
5	31	93.9	2195	2	T34264		hypothetical protein
6	31	93.9	2214	1	A48548		genomic polyprotein
7	30	90.9	1319	2	S30850		hypothetical protein
8	30	90.9	256	2	T0097		hypothetical protein
9	30	90.9	373	2	B70819		probable carnitine
10	30	90.9	383	2	T39854		hypothetical protein
11	30	90.9	478	2	A37430		calcitonin receptor

<http://es/ScoreAccessWeb/GetItem.action?ApplId=10510875&seqId=09323b67805b3ac6&itemName=200...>

<http://es/ScoreAccessWeb/GetItem.action?ApplId=10510875&seqId=0323b67805b3ac6&itemName=200...>

12	30	90.9	479	2	S33746		calcitonin receptor
13	30	90.9	515	2	I60000		hypothetical prote
14	30	90.9	617	2	T49059		probable cAMP-resp
15	30	90.9	699	2	T09639		glycoprotein B - b
16	30	90.9	874	2	S25530		ATP-dependent heli
17	30	90.9	946	2	F84280		probable membrane
18	30	90.9	1108	2	T35827		protein kinase (EC
19	29	87.9	124	2	S1670		hypothetical prote
20	29	87.9	185	2	E75311		SurP1 family prote
21	29	87.9	225	2	E87468		hypothetical prote
22	29	87.9	258	2	T21959		acetyl-CoA carboxy
23	29	87.9	262	2	G70001		seed albumin - mun
24	29	87.9	558127	2			hypothetical prote
25	29	87.9	276	2	T08773		2,5-diketo-D-gluc
26	29	87.9	277	1	A45961		acetyl-CoA carboxy
27	29	87.9	282	2	F84045		acetyl-CoA carboxy
28	29	87.9	294	2	AE1271		threonine synthase
29	29	87.9	294	2	AG1633		transcription regu
30	29	87.9	299	2	E81035		probable lsrR-fami
31	29	87.9	299	2	E81979		conserved hypothet
32	29	87.9	313	2	H69984		hypothetical prote
33	29	87.9	341	2	C81161		ferric enterobacti
34	29	87.9	347	2	A75265		threonine synthase
35	29	87.9	352	1	DMKTC		probable menE - My
36	29	87.9	362	2	A75364		hypothetical prote
37	29	87.9	379	2	A83404		metabolite transpo
38	29	87.9	427	2	B90371		UI snRNP 70K prote
39	29	87.9	427	2	S71367		hypothetical prote
40	29	87.9	427	2	D72379		conserved hypothet
41	29	87.9	435	2	E75395		1-aminoacylpropan
42	29	87.9	467	1	T7943		conserved hypothet
43	29	87.9	483	1	T7943		probable acetolact
44	29	87.9	488	2	F87443		acetolactate synth
45	29	87.9	490	2	G70806		hypothetical protein
46	29	87.9	515	2	S72987		hemocyanin chain a
47	29	87.9	515	2	T22790		hypothetical protein
48	29	87.9	614	1	B7TLA		hypothetical protein
49	29	87.9	631	1	E70895		hypothetical glyc

#### ALIGNMENTS

RESULT 1	gr15600	hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species:	Deinococcus radiodurans	
C:Date:	03-Dec-1999	#sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession:	H71600	
R:White, O ; Eisen, J.A. ; Heidelberg, J.F. ; Peterson, J.D. ; Dodson, R.J. ; Haft, D.H. ;		
Science 286, 1571-1577, 1999		
A:Title:	Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.	
A:Reference number:	A75250; MUID:2033696; PMID:10567266	
A:Accession:	H75600	
A:Status:	preliminary	
A:Molecule type:	DNA	
A:Residues:	1-223 <WHI>	
A:Cross-references:	UNIPROT:Q9RZ84 ; UNIPARC:UP1000000C1610 ; GB:AE001862 ;	
A:Experimental source:	strain R1	
A:Genetics:		
A:Map position:	2	
Query Match	100.0%	Score 33; DB 2; Length 223;

<http://es/ScoreAccessWeb/GetItem.action?ApplId=10510875&seqId=0323b67805b3ac6&itemName=200...>

<http://es/ScoreAccessWeb/GetItem.action?ApplId=10510875&seqId=09323b67805b3ac6&itemName=200...>

12/11/200

# SCORE Search Results Details for Application 10510875 and Search Result 20071207\_165338\_us-10-510-875a-7.dx.rup.

Score Home Page Retrieve Application List SCORE System.Overview SCORE\_EAO Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207\_165338\_us-10-510-875a-7.dx.rup.

Go Back to previous page

2M protein - protein search, using sw model

GenCore version 6.2.1  
(c) 1993 - 2007 Biocceleration Ltd.

Run on: December 7, 2007, 23:04:20 ; Search time 149 Seconds

(without alignments)  
77.206 Million cell updates/sec

Title: US-10-510-875A-7

Perfect score: 33

Sequence: 1 LXFAPG 7

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqS, 1645091341 residues

Total number of hits satisfying chosen parameters:

5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100\$

Listing first 50 summaries

Database : UniProt 12.1.1\*

1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*  
†

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB ID	Description
1	33	100.0	80	Q51M62_SILPO	Q51M62 silicibacter
2	33	100.0	105	Q7W59_CAEEL	Q7W59 caenorhabdii
3	33	100.0	161	Q4HJM3_9BACT	Q4hjm3 uncultured
4	33	100.0	161	Q4HJM6_9BACT	Q4hjm6 uncultured
5	33	100.0	161	Q4HJM2_9BACT	Q4hjm2 uncultured
6	33	100.0	161	Q4HJM4_9BACT	Q4hjm4 uncultured
7	33	100.0	161	Q4HJ01_9BACT	Q4hj01 uncultured
8	33	100.0	161	Q4HJM5_9BACT	Q4hjm5 uncultured

<http://escoreaccessweb/getitem.action?AppId=10510875&seqId=09323b67805b3ac8&itemName=200...> 12/11/200

9	33	100.0	161	Q4HJM7_9BACT	Q4hjm7 uncultured
10	33	100.0	161	Q4HJM6_9BACT	Q4hjm6 uncultured
11	33	100.0	197	A2ZJ15_ORYSI	A2zj15 oryza sativ
12	33	100.0	213	A5GK43_9DEL7	A5gk43 proteobacti
13	33	100.0	223	Q9RZ84_deiraa	Q9rz84 deinococcus
14	33	100.0	233	TNFA_DASNO	Tnfa_dasno
15	33	100.0	233	TNFA_TRITU	Tnfa_tritu
16	33	100.0	235	Q5W9H9_MERON	Q5w9h9 meronius un
17	33	100.0	236	AEGY31_FLAPU	Aegy31 flavobacter
18	33	100.0	248	Q85302_ARALP	Q85302 arabidopsis
19	33	100.0	254	ASFNCO_CYTJO	Asfnco flavobacter
20	33	100.0	264	Q0LDD4_herpetosiph	Q0ldd4 herpetosiph
21	33	100.0	288	Q13IY3_BURXL	Q13iy3 burkholderi
22	33	100.0	304	A1ISF3_GEOKN	A1isf3 geobacillus
23	33	100.0	304	Q5KVN9_GEOKA	Q5kvn9 geobacillus
24	33	100.0	315	Q5P4G9_AZ0SE	Q5p4g9 azospirillum
25	33	100.0	318	Q7TP9D9_ORYSI	Q7tp9d9 oryza sativ
26	33	100.0	322	Q650W6_ORYSI	Q650w6 oryza sativ
27	33	100.0	324	Q5LRF8_STLPO	Q5lrf8 silicibacte
28	33	100.0	337	Q0L1Z0_RALEJ	Q0l1z0 ralstonia e
29	33	100.0	338	Q46TC5_RALEJ	Q46tc5 ralstonia e
30	33	100.0	351	A2X7V0_ORYSI	A2x7v0 oryza sativ
31	33	100.0	351	Q1X8Q0_ORYSI	Q1x8q0 oryza sativ
32	33	100.0	372	A4BN04_9GAMM	A4bn04 nitrococcus
33	33	100.0	388	A4AE00_9ACTN	Aaero marine acti
34	33	100.0	400	A4U1L7_9EROT	A4u1l7 magnetospir
35	33	100.0	410	A1BJ58_ORYSI	A1bj58 oryza sativ
36	33	100.0	415	Q1DBF2_MYXXD	Q1dbf2 myxococcus
37	33	100.0	420	Q2JF04_FRA8C	Q2jf04 franria sp.
38	33	100.0	421	Q0JCY3_ORYSI	Q0jcy3 oryza sativ
39	33	100.0	429	Q0LM38_ORHAU	Q0lm38 herpetosiph
40	33	100.0	466	Q2EV24_HANP2	Q2ev24 xanthobacte
41	33	100.0	484	QEM6V5_CORG1	Qem6v5 corynebacte
42	33	100.0	491	Q93KPF1_CORG1	Q93kpf1 corynebacte
43	33	100.0	513	A0R519_MYCS2	A0r519 mycobacteri
44	33	100.0	516	A4QCH2_CORG8	A4qch2 corynebacte
45	33	100.0	615	A3TUR5_9RHOB	A3turs_9rhob
46	33	100.0	623	Q65576_ARATH	Q65576 arabidopsis
47	33	100.0	623	Q9BBB2_ARATH	Q9bbb2 arabidopsis
48	33	100.0	627	Q0BY76_HYPNA	Q0by76 hyphomonus
49	33	100.0	644	A0T012_9VTRU	A0t012_9vtru
50	33	100.0	653	Q1GNQ1_SPHAL	Q1gnq1 sphingopyxi

## ALIGNMENTS

RESULT 1	251M62_SILPO	Unreviewed;
ID	Q5LM62_SILPO	
AC	Q5LM62;	
DR	01-FEB-2005, integrated into UniProtKB/TREMBL.	
DT	01-FEB-2005, sequence version 1.	
DR	24-JUL-2007, entry version 10.	
DE	Putative, uncharacterized/Silicibacter.	
DN	Orderedocushnames-SP03J02;	
DS	Silicibacter pomeroyi.	
DC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;	
NCBI_TAXID	89184;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=ATCC 700808 / DSM 15171 / DS-3;	
RU	PubMed:15602564; DOI:10.1038/nature03170;	
RA	Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,	

<http://escoreaccessweb/getitem.action?AppId=10510875&seqId=09323b67805b3ac8&itemName=200...> 12/11/200

